

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Wei-Wu He, Kristine K. Kikly, Vishva M. Dixit, Steven M.

Ruben

(ii) TITLE OF THE INVENTION: INTERLEUKIN-1 BETA CONVERTING ENZYME LIKE APOPTOSIS PROTEASE-6

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: SmithKline Beecham Corporation
- (B) STREET: 709 Swedeland Road
- (C) CITY: King of Prussia
- (D) STATE: PA
- (E) COUNTRY: USA
- (F) ZIP: 19406-2799

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: UNKNOWN
- (B) FILING DATE: HEREWITH
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 60/018,961
- (B) FILING DATE: 05 JUNE 1996

- (A) APPLICATION NUMBER: 60/020,344
- (B) FILING DATE: 23 MAY 1996

- (A) APPLICATION NUMBER: 60/017,949
- (B) FILING DATE: 20 May 1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Han, William T.
 (B) REGISTRATION NUMBER: 34,344
 (C) REFERENCE/DOCKET NUMBER: P50483-2

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 610-270-5219
 (B) TELEFAX: 610-270-5090
 (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 416 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Asp	Glu	Ala	Asp	Arg	Arg	Leu	Leu	Arg	Arg	Cys	Arg	Leu	Arg	Leu
1															
															15
Val	Glu	Glu	Leu	Gln	Val	Asp	Gln	Leu	Trp	Asp	Val	Leu	Leu	Ser	Arg
															30
Glu	Leu	Phe	Arg	Pro	His	Met	Ile	Glu	Asp	Ile	Gln	Arg	Ala	Gly	Ser
															45
Gly	Ser	Arg	Arg	Asp	Gln	Ala	Arg	Gln	Leu	Ile	Ile	Asp	Leu	Glu	Thr
															60
Arg	Gly	Ser	Gln	Ala	Leu	Pro	Leu	Phe	Ile	Ser	Cys	Leu	Glu	Asp	Thr
															80
65															
Gly	Gln	Asp	Met	Leu	Ala	Ser	Phe	Leu	Arg	Thr	Asn	Arg	Gln	Ala	Gly
															95
85															
Lys	Leu	Ser	Lys	Pro	Thr	Leu	Glu	Asn	Leu	Thr	Pro	Val	Val	Leu	Arg
															110
100															
Pro	Glu	Ile	Arg	Lys	Pro	Glu	Val	Leu	Arg	Pro	Glu	Thr	Pro	Arg	Pro
															125
115															
Val	Asp	Ile	Gly	Ser	Gly	Gly	Phe	Gly	Asp	Val	Gly	Ala	Leu	Glu	Ser
130															
135															
140															

Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
 145 150 155 160
 Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
 165 170 175
 Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
 180 185 190
 Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
 195 200 205
 Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His
 210 215 220
 Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
 225 230 235 240
 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
 245 250 255
 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
 260 265 270
 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
 275 280 285
 Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
 290 295 300
 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
 305 310 315 320
 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
 325 330 335
 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
 340 345 350
 Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
 355 360 365
 Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu
 370 375 380
 Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
 385 390 395 400
 Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
 405 410 415

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1578 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCCATGGACG	AAGCGGATCG	GGCGCTCCTG	CGGCGGTGCC	GGCTGCGGCT	GGTGGAAAGAG	60
CTGCAGGTGG	ACCAAGCTCTG	GGACGTCCTG	CTGAGCCGCG	AGCTGTTCA	GCCCCATATG	120
ATCGAGGACA	TCCAGCGGGC	AGGCTCTGGA	TCTCGCGGG	ATCAGGCCAG	GCAGCTGATC	180
ATAGATCTGG	AGACTCGAGG	GAGTCAGGCT	CTTCCTTGT	TCATCTCCTG	CTTAGAGGAC	240
ACAGGCCAGG	ACATGCTGGC	TTCGTTCTG	CGAACTAAC	GCAGAACAGG	AAAGTTGTCG	300
AAGCCAACCC	TAGAAAACCT	TACCCCCAGTG	GTGCTCAGAC	CAGAGATTG	CAAACCAAGAG	360
GTTCTCAGAC	CGGAAACACC	CAGACCAGTG	GACATTGGTT	CTGGAGGATT	CGGTGATGTC	420
GGTGCTCTTG	AGAGTTGAG	GGGAAATGCA	GATTGGCTT	ACATCCTGAG	CATGGAGCCC	480
TGTGGCCACT	GCCTCATTAT	CAACAATGTG	AACTTCAGCC	GTGAGTCCGG	GCTCCGCACC	540
CGCACTGGCT	CCAACATCGA	CTGTGAGAAG	TTGCGCGTC	GCTTCTCCTC	GCTGCATTTC	600
ATGGTGGAGG	TGAAGGGCGA	CCTGACTGCC	AAGAAAATGG	TGCTGGCTT	GCTGGAGCTG	660
GCGCGGCAGG	ACCACGGTGC	TCTGGACTGC	TGCGTGGTGG	TCATTCTCTC	TCACGGCTGT	720
CAGGCCAGCC	ACCTGCAGTT	CCCAGGGCT	GTCTACGGCA	CAGATGGATG	CCCTGTGTCG	780
GTCGAGAAGA	TTGTGAACAT	CTTCAATGGG	ACCAGCTGCC	CCAGCCTGGG	AGGGAAAGCCC	840
AAGCTCTTT	TCATCCAGGC	CTGTGGTGGG	GAGCAGAAAG	ACCATGGGTT	TGAGGTGGCC	900
TCCACTTCCC	CTGAAGACGA	GTCCCCTGGC	AGTAACCCCG	AGCCAGATGC	CACCCCGTTC	960
CAGGAAGGTT	TGAGGACCTT	CGACCAGCTG	GACGCCATAT	CTAGTTGCC	CACACCCAGT	1020
GACATCTTG	TGTCCTACTC	TACTTTCCA	GGTTTTGTTT	CCTGGAGGGA	CCCCAAGAGT	1080
GGCTCCTGGT	ACGTTGAGAC	CCTGGACGAC	ATCTTGAGC	AGTGGGCTCA	CTCTGAAGAC	1140
CTGCAGTC	CCCTGCTTAG	GGTCGCTAAT	GCTGTTTCGG	TGAAAGGGAT	TTATAAACAG	1200
ATGCCTGGTT	GCTTTAATT	CCTCCGAAA	AAACTTTCT	TTAAAACATC	ATAAGGCCAG	1260
GGCCCTCAC	CCTGCCTTAT	CTTGACCCCC	AAAGCTTTCC	TGCCCCAGGC	CTGAAAGAGG	1320
CTGAGGCC	GACTTCCTG	CAACTCAAGG	ACTTTGNAGC	CGGCACAGGG	TCTGCTCTTT	1380
CTCTGCCAGT	GACACACAGG	CTCTTAGCAG	CTTCCAGATT	GACGACAAGT	GCTGAACAGT	1440
GGAGGAAGAG	GGACAGATGA	ATGCCGTGGA	TTGCACGTGG	NCTCTTGAGC	AGTGGCTGGT	1500
CCAGGGCTAG	TGACTTGGTG	TCCCATGATC	CCTGTGTTGG	TCTCTAGGAG	CAGGGATTAA	1560
CCTCTGCACT	ACTGACAT					1578

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 639 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGACTGCCA AGAAAATGGT GCTGGCTTG CTGGAGCTGG CGCGGCAGGA CCACGGTGCT	60
CTGGACTGCT GCGTGGTGGT CATTCTCTCT CACGGCTGTC AGGCCAGCCA CCTGCAGTTC	120
CCAGGGGCTG TCTACGGCAC AGATGGATGC CCTGTGTCGG TCGAAAAGAT TGTGAACATC	180
TTCAATGGGA CCAGCTGCC CAGCCTGGGA GGGAAAGCCCA AGCTCTTTT CATCCAGGCC	240
TGTGGTGGGG AGCAGAAAGA CCATGGGTTT GAGGTGGCCT CCACCTCCCC TGAAGACGAG	300
TCCCCTGGCA GTAACCCCCGA GCCAGATGCC ACCCCGTTCC AGGAAGGTTT GAGGACCTTC	360
GACCAGCTGG ACGCCATATC TAGTTTGCCC ACACCCAGTG ACATCTTGT GTCCTACTCT	420
ACTTTCCCAG GTTTTGTTC CTGGAGGGAC CCCAAGAGTG GCTCCTGGTA CGTTGAGACC	480
CTGGACGACA TCTTGAGCA GTGGGCTCAC TCTGAAGACC TGCAGTCCCT CCTGCTTAGG	540
GTCGCTAATG CTGTTTCGGT GAAAGGGATT TATAAACAGA TGCCTGGTTG CTTTAATTTC	600
CTCCGGAAAA AACTTTCTT TTAAAACATC ATAAGGCAG	639

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 203 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His Gly Ala Leu			
1	5	10	15
Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln Ala Ser His			
20	25	30	
Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys Pro Val Ser			
35	40	45	
Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys Pro Ser Leu			
50	55	60	
Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly Glu Gln			

65	70	75	80
Lys			
Asp			
His			
Gly			
Phe			
Glu			
Val			
Ala			
Ser			
Thr			
Ser			
Pro			
Glu			
Asp			
Gly			
Ser			
Asn			
Pro			
Glu			
Pro			
Asp			
Ala			
Thr			
Pro			
Phe			
Gly			
Leu			
Asp			
Ala			
Ile			
Ser			
Ser			
Leu			
Pro			
Thr			
Pro			
Ser			
Asp			
Ile			
Phe			
Val			
Ser			
Tyr			
Ser			
Thr			
Phe			
Pro			
Gly			
Phe			
Val			
Ser			
Trp			
Arg			
Asp			
Ile			
Phe			
Val			
Ser			
Tyr			
Ser			
Thr			
Phe			
Pro			
Gly			
Phe			
Val			
Ser			
Trp			
Arg			
Gly			
Ile			
Tyr			
Lys			
Gln			
Met			
Pro			
Gly			
Cys			
Ala			
Asn			
Ala			
Val			
Ser			
Val			
Lys			
Gly			
Ile			
Tyr			
Lys			
Gln			
Met			
Pro			
Gly			
Cys			
Phe			
Asn			
Phe			
Leu			
Arg			
Lys			
Lys			
Leu			
Phe			
Met			
195	196	197	198

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAACGGGGTA CCGCCATGGA CGAACGGGAT CGGC

34

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGCTCTAGAT TAGTGGTGGT GGTGGTGGTG TGATGTTTA AAGAAAAGTT TTTTCCGGAG

60

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCTCTTT TCATCCAGGC CGCGGGTGGG GAGCAGAAGA C

41

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCTTCTGC TCCCCACCCG CGGCCTGGAT GAAAAAAGC

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGCTCTAGAT TAC TTGTCAT CGTCGTCCTT GTAGTCTGAT GTTTTAAAGT TAAGTTTTTT

60

66

CCGGAG

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: DIXIT, VISHVA M.
HE, WEI-WU
KIKLY, KRISTINE K.
RUBEN, STEVEN M.

(ii) TITLE OF THE INVENTION: INTERLEUKIN-1 BETA CONVERTING
ENZYME LIKE APOPTOTIC PROTEASE-6

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Ratner & Prestia
(B) STREET: P.O. Box 980
(C) CITY: Valley Forge
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19482

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/352,936
(B) FILING DATE: 08-MAY-1997
(C) CLASSIFICATION: UNKNOWN

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/013,961
(B) FILING DATE: 05-JUN-1996

(A) APPLICATION NUMBER: 60/020,344
(B) FILING DATE: 23-MAY-1996

(A) APPLICATION NUMBER: 60/017,949
(B) FILING DATE: 20-MAY-1996

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Prestia, Paul F
(B) REGISTRATION NUMBER: 23,031
(C) REFERENCE/DOCKET NUMBER: p50483-2

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 610-407-0700
(B) TELEFAX: 610-407-0700
(C) TELEX: 346163

(x) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Asp Glu Ala Asp Arg Arg Leu Leu Arg Arg Cys Arg Leu Arg Leu
 15
 1 5 10 15
 Val Glu Glu Leu Gln Val Asp Gln Leu Trp Asp Val Leu Leu Ser Arg
 20 25 30
 Glu Leu Phe Arg Pro His Met Ile Glu Asp Ile Gln Arg Ala Gly Ser
 35 40 45
 Gly Ser Arg Arg Asp Gln Ala Arg Gln Leu Ile Asp Leu Glu Thr
 50 55 60
 Arg Gly Ser Gln Ala Leu Pro Leu Phe Ile Ser Cys Leu Glu Asp Thr
 65 70 75 80
 Gly Gln Asp Met Leu Ala Ser Phe Leu Arg Thr Asn Arg Gln Ala Gly
 85 90 95
 Lys Leu Ser Lys Pro Thr Leu Glu Asn Leu Thr Pro Val Val Leu Arg
 100 105 110
 Pro Glu Ile Arg Lys Pro Glu Val Leu Arg Pro Glu Thr Pro Arg Pro
 115 120 125
 Val Asp Ile Gly Ser Gly Gly Phe Asp Val Gly Ala Leu Glu Ser
 130 135 140
 Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
 145 150 155 160
 Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
 165 170 175
 Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
 180 185 190
 Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
 195 200 205
 Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His
 210 215 220
 Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
 225 230 235 240
 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
 245 250 255
 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
 260 265 270
 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
 275 280 285
 Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
 290 295 300
 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
 305 310 315 320
 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
 325 330 335
 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
 340 345 350
 Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
 355 360 365
 365

Asp Ile Phe Glu Gin 370 Ala His Ser Glu Asp Leu Gln Ser Ile Leu
 375 380
 Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
 385 390 395 400
 Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
 405 410 415
 405

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCATGGACG AAGCGGATCG GCGGCTCCTG	CGGCGGTGCC GGCTGCGGCT	GGTGGAAAGAG	60
CTGCAGGTGG ACCAGCTCTG GGACGCTCCTG	CTGAGCCGGG AGCTGTTCTG	GCCCCATATG	120
ATCGAGGACA TCCAGCGGGC AGGCTCTGGA	ATCAGGCGGG ATCAGGCGAG	GCAGCTGATC	180
ATAGATCTGG AGACTCGAGG GAGTCAGGCT	CTTCCTTTGT TCATCTCTG	CTTAGAGGAC	240
ACAGGCCAGG ACATGCTGGC TTGCTTCTG CGAACATAACA	GGCAAGCAGG AAAGTTGTCG	300	
AAGCCAAACCC TAGAAAACCT TACCCCCAGTG	GTGCTCAGAC CAGAGATTCG	CAAACCAGAG	360
GTTCTCAGAC CGGAAACACC CAGACCAGTG	GACATTGGTT CTGGAGGATT	CGGTGATGTC	420
GGTGCTCTTG AGAGTTTGAG GGGAAATGCA	GATTGGCTT ACATCCTGAG	CATGGAGCCC	480
TGTGGCCACT GCCTCATTAT CAAACATGTG	GTGAGTCGGG GCTCCGCACC	540	
CGCACTGGCT CCAACATCGA CTGTGAGAAG	TTGCGGGCGTC GTTCTCCTC	GCTGCATTTC	600
ATGGTGGAGG TGAAGGGCGA CCTGACTGCC	AAGAAAATGG TGCTGGCTTT	GCTGGAGCTG	660
GCGCGGCAGG ACCACGGGTGC TCTGGACTGC	TGCCTGGTGG TCATTCTCTC	TCACGGCTGT	720
CAGGCCAGCC ACCTGCAGTT CCCAGGGCT	GTCTACGGCA CAGATGGATG	CCCTGTGTCTG	780
GTCGAGAAGA TTGTGAACAT CTTCAATGGG	ACCAGCTGCC CCAGCCTGGG	AGGGAAAGCCC	840
AAGCTCTTT TCATCCAGGC CTGTGGTGGG	GAGCAGAAAG ACCATGGGTT	TGAGGTGGCC	900
TCCACTTCCC CTGAAGACGA GTCCCCCTGGC	AGTACCCCCG AGCCAGATGC	CACCCCGTTC	960
CAGGAAGGTT TGAGGACCTT CGACCAAGCTG	CTAGTTGCC CACACCCAGT	1020	
GACATCTTTG TGTCTTACTC TACTTTCCA	CGTTTTGTTT CCTGGAGGGA	CCCCAAGAGT	1080
GGCTCCTGGT ACGTTGAGAC CCTGGACGAC	ATCTTTGAGC AGTGGGCTCA	CTCTGAAGAC	1140
CTGCAGTCCC TCCTGCTTAG GGTGCGTAAT	GCTGTTTCGG TGAAAGGGAT	TTATAAACAG	1200
ATGCCCTGGTT GCTTTAATTG CCTCCGGAAA	AAACTTTCT TTAAAACATC	ATAAGGCCAG	1260
GGCCCCCTCAC CCTGCCTTAT CTTGCACCCCC	AAAGCTTTCC TGCCCCAGGC	CTGAAAGAGG	1320
CTGAGGCCTG GACTTTCTG CAACTCAAGG	CGGCACAGGG TCTGCTCTT	1380	
CTCTGCCAGT GACAGACAGG CTCTTAGCAG	CTTCCAGATT GACGACAAGT	GCTGAACAGT	1440
GGAGGAAGAG GGACAGATGA ATGCCGTGGA	NCTCTTGAGC AGTGGCTGGT	1500	
CCAGGGCTAG TGACTTGGTG TCCCATGATC	CCTGTGTTGG TCTCTAGGAG	CAGGGATTA	1560
CCTCTGCACT ACTGACAT			1578

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGACTGCCA	AGAAAATGGT	GCTGGCTTTG	CTGGAGCTGG	CCCGGCAGGA	CCACGGTGCT	60
CTGGACTGCT	GGGTGGTGGT	CATTCTCTCT	CACGGCTGTC	AGGCCAGCCA	CCTGCAGTTC	120
CCAGGGGCTG	TCTACGGCAC	AGATGGATGC	CCTGTGTCGG	TGGAAAAGAT	TGTGAACATC	180
TTCAATGGGA	CCAGCTGCC	CAGCCTGGGA	GGGAAGCCCCA	AGCTCTTTT	CATCCAGGCC	240
TGTGGTGGGG	AGCAGAAAGA	CCATGGGTTT	GAGGTGGCCT	CCACTTCCCC	TGAAGACGAG	300
TCCCCTGGCA	GTAACCCCGA	GCCAGATGCC	ACCCCGTTCC	AGGAAGGTTT	GAGGACCTTC	360
GACCAGCTGG	ACGCCATATC	TAGTTTGC	ACACCCAGTG	ACATCTTGT	GTCCTACTCT	420
ACTTTCCCAG	GT	TTTGTTC	CCCAAGAGTG	GCTCCGGTA	CGTTGAGACC	480
CTGGACGACA	TCTTGAGCA	GTGGGCTCAC	TCTGAAGACC	TGCAGTC	CCTGCTTAGG	540
GTCGCTAATG	CTGTTTCGGT	GAAAGGGATT	TATAAACAGA	TGCCTGGTTG	CTTTAATTTC	600
CTCCGGAAAA	AACTTTCTT	TTAAACACATC	ATAAGGCAG			639

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His Gly Ala Leu						
1	5	10	15			
Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln Ala Ser His						
20	25	30				
Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys Pro Val Ser						
35	40	45				
Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys Pro Ser Leu						
50	55	60				
Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly Glu Gln						
65	70	75	80			
Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu Asp Glu Ser						
85	90	95				
Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln Glu Gly Leu						
100	105	110				
Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro Thr Pro Ser						
115	120	125				
Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val Ser Trp Arg						
130	135	140				
Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp Asp Ile Phe						
145	150	155	160			
Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu Leu Arg Val						
165	170	175				
Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met Pro Gly Cys						
180	185	190				
Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Met						
195	200					

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAACGGGGTA CCGCCATGGA CGAACGCGAT CGGC

34

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGCTCTAGAT TAGTGGTGGT GGTGGTGGTG TGATTTTA AAGAAAAGTT TTTTCCGGAG

60

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCTCTTTT TCATCCAGGC CGCGGGTGGG GAGCAGAAGA C

41

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCTTTCTGC TCCCCACCCG CGGCCTGGAT GAAAGAAGC

39

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGCTCTAGAT TACTTGTCAT CGTCGTCCTT GTAGTCTGAT GTTTTAAAGT TAAGTTTTT
CCGGAG

60

66

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Ala Cys Arg Gly
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gln Ala Cys Gly Gly
1 5